

IN THE SPECIFICATION

Please amend the specification as follows.

On page 21, please amend the paragraph on lines 12-23 as follows.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., *J. Mol. Biol.* **215**, 403-410, (1990) and Karlin et al., *Proc. Natl. Acad. Sci. USA* **90**, 5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., *Methods in Enzymology*, **266**, 460-480 (1996); ~~http://blast.wustl.edu/blast/~~ README.html. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

On page 29, please amend the paragraph on lines 22-32 as follows.

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (*e.g.*, CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC; ~~Bethesda, Md.~~ 10801 University Boulevard, Manassas, VA 20110-2209) and may be chosen to ensure the correct modification and processing of the foreign protein.